Amended page 51, paragraph from lines 1-12:

FIG. 16 presents the nucleotide sequence of the genomic region of the *hpa* gene with regard to SEQ ID NO: 42.   Exon sequences appear in upper case and intron sequences in lower case. The deduced amino acid sequence of the exons is printed below the nucleotide sequence. Two predicted transcription start sites are shown in bold.

FIG. 17 presents an alignment of the amino acid sequences of human heparanase, mouse and partial sequences of rat homologues with regard to SEQ ID NOs: 10, 44 and 45. The human and the mouse sequences were determined by sequence analysis of the isolated cDNAs. The rat sequence is derived from two different EST clones, which represent two different regions (5' and 3') of the rat *hpa* cDNA. The human sequence and the amino acids in the mouse and rat homologues, which are identical to the human sequence, appear in bold.

β2

Amendment of page 52, lines 1-5:

FIG. 19 demonstrates the secondary structure prediction for heparanase (SEQ ID NO:10) performed using the PHD server – Profile network Prediction Heidelberg. H – helix, E – extended (beta strand), The glutamic acid predicted as the proton donor is marked by asterisk and the possible nucleophiles are underlined.

β3

2